

Remarks

The specification has been amended to correctly respect trademarks, using capitalization for the mark and an accompanying generic term.

The status identifiers of claims 1 and 16 have been corrected and the changes in the claims from the original properly indicated.

Sequence identifiers have been inserted in each of claims 4-6 and 19-21.

Claims 1 and 16 were amended to provide the originally named genus of bacterium taught in the specification. This amendment addresses the rejection for new matter.

The pending claims are rejected as indefinite and unclear. This rejection is respectfully traversed. The Office Action states that it is unclear what segment of the *S. aureus* 16S rRNA gene the primers are actually amplifying. In the presence of a template from *S. aureus*, the primers amplify a segment that comprises a conserved region and a divergent region. The conserved region and the divergent region are defined by similarity to at least 10 eubacterial species (conserved) or divergence from *Bradyrhizobium japonicum* (divergent), respectively. *S. aureus* 16S rRNA gene contains more than one such segment, but not any segment of the gene will fulfill these criteria. An example of one such segment is recited in claim 4, i.e., nucleotides 890 to 1051.


The method of the present claims does not recite or specify the amplifying of a segment of a *S. aureus* 16S rRNA gene. The ability to amplify *S. aureus* 16S rRNA gene is a property of the primers. The recited step of "amplifying template DNA" does not specify that the template DNA is from *S. aureus*. The template DNA which is amplified can be from any eubacteria. In fact, the purpose of the method is to detect and determine species of a eubacteria (which may be unidentified at the outset of the assay) by virtue of detecting and amplifying its rRNA.

It is respectfully submitted that the claims are clear and definite as they are currently framed. Withdrawal of this rejection is respectfully requested.

Respectfully submitted,

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